

SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> Rad2/FEN-1 Orthologues and Uses
Thereof

<130> 0961D

<150> 09/426,557

<151> 1999-10-22

<150> 60/112,332

<151> 1998-12-15

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<170> FastSEQ for Windows Version 3.0

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<211> 1463

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (85)...(1221)

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Met Gly Ile Lys Gly Leu Thr Lys Leu	
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ctg gcg gac aat gcg ccc aag gcg atg aag gag cag aag ttc gag agc	159
Leu Ala Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys Phe Glu Ser	
10 15 20 25	
tac ttc ggc cgc aaa atc gcc gtc gac gcc agc atg agc ata tac cag	207
Tyr Phe Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln	
30 35 40	
ttc ctg att gta gtt gga agg aca ggc atg gaa act ctc aca aat gaa	255
Phe Leu Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu	
45 50 55	
gct ggt gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata	303
Ala Gly Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile	
60 65 70	
aga tta ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat ggc aag	351
Arg Leu Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys	
75 80 85	
cct cct gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga	399
Pro Pro Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg	
90 95 100 105	
gat gat gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa	447
Asp Asp Ala Thr Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys	

110	115	120	
gat gcg att gaa aaa ttg agc aag agg act gta aag gtc aca agg caa Asp Ala Ile Glu Lys Leu Ser Lys Arg Thr Val Lys Val Thr Arg Gln 125 130 135			495
cac aac gaa gat tgt aaa cgg cta tta aga ctt atg ggg gtt cct gtt His Asn Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly Val Pro Val 140 145 150			543
gta gag gca cct tct gaa gca gaa gca gaa tgt gca gcc ctt tgc ata Val Glu Ala Pro Ser Glu Ala Glu Ala Glu Cys Ala Ala Leu Cys Ile 155 160 165			591
aac gat aag gtg ttc gct gtt gct tca gaa gat atg gac tcc ctt act Asn Asp Lys Val Phe Ala Val Ala Ser Glu Asp Met Asp Ser Leu Thr 170 175 180 185			639
ttt ggg gct cca cgg ttc ctt cgt cat tta atg gat cca agt tcc aag Phe Gly Ala Pro Arg Phe Leu Arg His Leu Met Asp Pro Ser Ser Lys 190 195 200			687
aaa ata cct gtg atg gaa ttt gat gtt gcc aag gtt ttg gag gag ctt Lys Ile Pro Val Met Glu Phe Asp Val Ala Lys Val Leu Glu Glu Leu 205 210 215			735
gaa ctc acc atg gac cag ttc att gat ttg tgc atc ctg tgt gga tgt Glu Leu Thr Met Asp Gln Phe Ile Asp Leu Cys Ile Leu Cys Gly Cys 220 225 230			783
gac tat tgt gat agc atc aaa ggt atc ggg ggg caa aca gct ctg aaa Asp Tyr Cys Asp Ser Ile Lys Gly Ile Gly Gly Gln Thr Ala Leu Lys 235 240 245			831
ctt att cgt caa cat ggg tcc ata gaa agc atc ttg gag aat ctt aat Leu Ile Arg Gln His Gly Ser Ile Glu Ser Ile Leu Glu Asn Leu Asn 250 255 260 265			879
aaa gac aga tat caa att cct gag gac tgg cct tac caa gaa gct cga Lys Asp Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln Glu Ala Arg 270 275 280			927
cgc ttg ttc aag gag cct aat gtc aca ttg gat att cct gag cta aaa Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro Glu Leu Lys 285 290 295			975
tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg gta aaa gat Trp Thr Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu Val Lys Asp 300 305 310			1023
aat ggt ttc aac gaa gat cgg gtg aca aag gcc ata gag aag atc aaa Asn Gly Phe Asn Glu Asp Arg Val Thr Lys Ala Ile Glu Lys Ile Lys 315 320 325			1071
tct gcc aag aat aaa tcg tcg caa gga aga ctc gag tcc ttt ttc aag Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser Phe Phe Lys 330 335 340 345			1119
cca act gcc acc aca tca gca ccg cta aaa cgg aag gag act tcg gat Pro Thr Ala Thr Thr Ser Ala Pro Leu Lys Arg Lys Glu Thr Ser Asp 350 355 360			1167

aaa aca agc aag gca gct gcg aac aag aaa aca aag gct ggt gga aag 1215
 Lys Thr Ser Lys Ala Ala Ala Asn Lys Lys Thr Lys Ala Gly Gly Lys
 365 370 375

aag aaa taatcttgga tgcttgatgt acaactacga ctacgaaagc agcgggtggcg 1271
 Lys Lys

tgatcacttc gottagatta tttaactccc tgttttaact cagagctttg gtaaaagttt 1331
 gtcctatgttt caagctgggg taagtttagtt gtgtttgaag agattgggtgt accaagtaac 1391
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 <213> Zea mays

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Val	Asp	Ala	Ser	Met	Ser	Ile	Tyr	Gln	Phe	Leu	Ile	Val	Val	Gly	Arg
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Thr	Gly	Met	Glu	Thr	Leu	Thr	Asn	Glu	Ala	Gly	Glu	Val	Thr	Ser	His
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Leu	Gln	Gly	Met	Phe	Asn	Arg	Thr	Ile	Arg	Leu	Leu	Glu	Ala	Gly	Ile
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Lys	Pro	Val	Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Asp	Met	Lys	Lys	Gln
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Glu	Leu	Ala	Lys	Arg	Tyr	Ser	Lys	Arg	Asp	Asp	Ala	Thr	Lys	Asp	Leu
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Thr	Glu	Ala	Val	Glu	Val	Gly	Asp	Lys	Asp	Ala	Ile	Glu	Lys	Leu	Ser
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Lys	Arg	Thr	Val	Lys	Val	Thr	Arg	Gln	His	Asn	Glu	Asp	Cys	Lys	Arg
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Leu	Leu	Arg	Leu	Met	Gly	Val	Pro	Val	Val	Glu	Ala	Pro	Ser	Glu	Ala
				145		150				155					160
Glu	Ala	Glu	Cys	Ala	Ala	Leu	Cys	Ile	Asn	Asp	Lys	Val	Phe	Ala	Val
				165					170					175	
Ala	Ser	Glu	Asp	Met	Asp	Ser	Leu	Thr	Phe	Gly	Ala	Pro	Arg	Phe	Leu
			180					185					190		
Arg	His	Leu	Met	Asp	Pro	Ser	Ser	Lys	Lys	Ile	Pro	Val	Met	Glu	Phe
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Asp	Val	Ala	Lys	Val	Leu	Glu	Glu	Leu	Glu	Leu	Thr	Met	Asp	Gln	Phe
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Ile	Asp	Leu	Cys	Ile	Leu	Cys	Gly	Cys	Asp	Tyr	Cys	Asp	Ser	Ile	Lys
				225		230				235					240
Gly	Ile	Gly	Gly	Gln	Thr	Ala	Leu	Lys	Leu	Ile	Arg	Gln	His	Gly	Ser
				245					250					255	
Ile	Glu	Ser	Ile	Leu	Glu	Asn	Leu	Asn	Lys	Asp	Arg	Tyr	Gln	Ile	Pro
			260				265						270		
Glu	Asp	Trp	Pro	Tyr	Gln	Glu	Ala	Arg	Arg	Leu	Phe	Lys	Glu	Pro	Asn
			275				280						285		
Val	Thr	Leu	Asp	Ile	Pro	Glu	Leu	Lys	Trp	Thr	Ala	Pro	Asp	Glu	Glu
			290			295					300				
Gly	Leu	Ile	Ser	Phe	Leu	Val	Lys	Asp	Asn	Gly	Phe	Asn	Glu	Asp	Arg
					305		310			315					320

Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
325 330 335
Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
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Pro Leu Lys Arg Lys Glu Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala
355 360 365
Asn Lys Lys Thr Lys Ala Gly Gly Lys Lys Lys
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acagccgccg cagacgag atg ggc atc aag ggt ttg acg aaa ctg ctg gcg 111
Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala
1 5 10
gac aat gcg ccc aag gcg atg aag gag cag aag ttc gag agc tac ttc 159
Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe
15 20 25
ggc cgc aaa atc gcc gtc gac gcc agc atg agc ata tac cag ttc ctg 207
Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu
30 35 40
att gta gtt gga agg aca ggc atg gaa act ctc aca aat gaa gct ggt 255
Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly
45 50 55
gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata aga tta 303
Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu
60 65 70 75
ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat ggc aag cct cct 351
Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro
80 85 90
gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga gat gat 399
Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp
95 100 105
gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa gat gcg 447
Ala Thr Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala
110 115 120
att gaa aaa ttg agc aag agg act gta aag gtc aca agg caa cac aac 495
Ile Glu Lys Leu Ser Lys Arg Thr Val Lys Val Thr Arg Gln His Asn
125 130 135
gaa gat tgt aaa cgg cta tta aga ctt atg ggg gtt cct gtt gta gag 543
Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly Val Pro Val Val Glu
140 145 150 155
gca cct tct gaa gca gaa gca gaa tgt gca gcc ctt tgc ata aac gat 591

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<400> 4

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Val	Asp	Ala	Ser	Met	Ser	Ile	Tyr	Gln	Phe	Leu	Ile	Val	Val	Gly	Arg
	35						40					45			
Thr	Gly	Met	Glu	Thr	Leu	Thr	Asn	Glu	Ala	Gly	Glu	Val	Thr	Ser	His
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Leu	Gln	Gly	Met	Phe	Asn	Arg	Thr	Ile	Arg	Leu	Leu	Glu	Ala	Gly	Ile
65					70					75					80
Lys	Pro	Val	Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Asp	Met	Lys	Lys	Gln
				85					90					95	
Glu	Leu	Ala	Lys	Arg	Tyr	Ser	Lys	Arg	Asp	Asp	Ala	Thr	Lys	Asp	Leu
			100					105						110	
Thr	Glu	Ala	Val	Glu	Val	Gly	Asp	Lys	Asp	Ala	Ile	Glu	Lys	Leu	Ser
	115						120					125			
Lys	Arg	Thr	Val	Lys	Val	Thr	Arg	Gln	His	Asn	Glu	Asp	Cys	Lys	Arg
	130					135					140				
Leu	Leu	Arg	Leu	Met	Gly	Val	Pro	Val	Val	Glu	Ala	Pro	Ser	Glu	Ala
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Glu	Ala	Glu	Cys	Ala	Ala	Leu	Cys	Ile	Asn	Asp	Lys	Val	Phe	Ala	Val
			165						170					175	
Ala	Ser	Glu	Asp	Met	Asp	Ser	Leu	Thr	Phe	Gly	Ala	Pro	Arg	Phe	Leu
			180					185					190		
Arg	His	Leu	Met	Asp	Pro	Ser	Ser	Lys	Lys	Ile	Pro	Val	Met	Glu	Phe
	195					200						205			
Asp	Val	Ala	Lys	Val	Leu	Glu	Glu	Leu	Glu	Leu	Thr	Met	Asp	Gln	Phe
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Ile	Asp	Leu	Cys	Ile	Leu	Cys	Gly	Cys	Asp	Tyr	Cys	Asp	Ser	Ile	Lys
225					230					235					240
Gly	Ile	Gly	Gly	Gln	Thr	Ala	Leu	Lys	Leu	Ile	Arg	Gln	His	Gly	Ser
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Ile	Glu	Ser	Ile	Leu	Glu	Asn	Leu	Asn	Lys	Asp	Arg	Tyr	Gln	Ile	Pro
		260					265						270		
Glu	Asp	Trp	Pro	Tyr	Gln	Glu	Ala	Arg	Arg	Leu	Phe	Lys	Glu	Pro	Asn
	275						280					285			
Val	Thr	Leu	Asp	Ile	Pro	Glu	Leu	Lys	Trp	Thr	Ala	Pro	Asp	Glu	Glu
	290					295					300				
Gly	Leu	Ile	Ser	Phe	Leu	Val	Lys	Asp	Asn	Gly	Phe	Asn	Glu	Asp	Arg
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Val	Arg	Lys	Ala	Ile	Glu	Lys	Ile	Lys	Ser	Ala	Lys	Asn	Lys	Ser	Ser
			325						330					335	
Gln	Gly	Arg	Leu	Glu	Ser	Phe	Phe	Lys	Pro	Thr	Ala	Thr	Thr	Ser	Ala
			340					345					350		
Pro	Leu	Lys	Arg	Lys	Glu	Thr	Ser	Asp	Lys	Thr	Ser	Lys	Ala	Ala	Ala
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Asn	Lys	Lys	Thr	Lys	Ala	Gly	Gly	Lys	Lys	Lys					
370						375									

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Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys		
	10 15 20	
ttc gag agc tac ttc ggc cgc aaa atc gcc gtc gac gcc agc atg agc	150	
Phe Glu Ser Tyr Phe Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser		
	25 30 35	
ata tac cag ttc ctg att gta gtt gga agg aca ggc atg gaa act ctc	198	
Ile Tyr Gln Phe Leu Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu		
	40 45 50	
aca aat gaa gct ggt gaa gtc act agt cat ttg caa gga atg ttc aac	246	
Thr Asn Glu Ala Gly Glu Val Thr Ser His Leu Gln Gly Met Phe Asn		
	55 60 65 70	
cgg aca ata aga tta ctg gaa gcg gga atc aag cca gtt tat gtt ttt	294	
Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe		
	75 80 85	
gat ggc aag cct cct gat atg aag aaa caa gag ctt gct aaa aga tac	342	
Asp Gly Lys Pro Pro Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr		
	90 95 100	
tca aaa aga gat gat gca acc aaa gat ctg act gag gca gta gag gta	390	
Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu Thr Glu Ala Val Glu Val		
	105 110 115	
gga gat aaa gat gcg att gaa aaa ttg agc aag agg act gta aag gtc	438	
Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser Lys Arg Thr Val Lys Val		
	120 125 130	
aca agg caa cac aac gaa gat tgt aaa cgg cta tta aga ctt atg ggg	486	
Thr Arg Gln His Asn Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly		
	135 140 145 150	
gtt cct gtt gta gag gca cct tct gaa gca gaa gca gaa tgt gca gcc	534	
Val Pro Val Val Glu Ala Pro Ser Glu Ala Glu Ala Glu Cys Ala Ala		
	155 160 165	
ctt tgc ata aac gat aag gtg ttc gct gtt gct tca gaa gat atg gac	582	
Leu Cys Ile Asn Asp Lys Val Phe Ala Val Ala Ser Glu Asp Met Asp		
	170 175 180	
tcc ctt act ttt ggg gct cca cgg ttc ctt cgt cat tta atg gat cca	630	
Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu Arg His Leu Met Asp Pro		
	185 190 195	
agt tcc aag aaa ata cct gtg atg gaa ttt gat gtt gcc aag gtt ttg	678	
Ser Ser Lys Lys Ile Pro Val Met Glu Phe Asp Val Ala Lys Val Leu		
	200 205 210	

gag gag ctt gaa ctc acc atg gac cag ttc att gat ttg tgc atc ctg	726
Glu Glu Leu Glu Leu Thr Met Asp Gln Phe Ile Asp Leu Cys Ile Leu	
215 220 225 230	
tgt gga tgt gac tat tgt gat agc atc aaa ggt atc ggg ggg caa aca	774
Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys Gly Ile Gly Gly Gln Thr	
235 240 245	
gct ctg aaa ctt att cgt caa cat ggg tcc ata gaa agc atc ttg gag	822
Ala Leu Lys Leu Ile Arg Gln His Gly Ser Ile Glu Ser Ile Leu Glu	
250 255 260	
aat ctt aat aaa gac aga tat caa att cct gag gac tgg cct tac caa	870
Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln	
265 270 275	
gaa gct cga cgc ttg ttc aag gag cct aat gtc aca ttg gat att cct	918
Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro	
280 285 290	
gag cta aaa tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg	966
Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu	
295 300 305 310	
gta aaa gat aat ggt ttc aac gaa gat cgg gtg aca aag gcc ata gag	1014
Val Lys Asp Asn Gly Phe Asn Glu Asp Arg Val Thr Lys Ala Ile Glu	
315 320 325	
aag atc aaa tct gcc aag aat aaa tcg tcg caa gga aga ctc gag tcc	1062
Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser	
330 335 340	
ttt ttc aag cca act gcc acc aca tca gca ccg cta aaa cgg aag gag	1110
Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala Pro Leu Lys Arg Lys Glu	
345 350 355	
act tcg gat aaa aca agc aag gca gct gcg aac aag aaa aca aag gct	1158
Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala Asn Lys Lys Thr Lys Ala	
360 365 370	
ggt gga aag aag aaa taatcttgga tgcttgatgt acaactacga ctacgaaagc	1213
Gly Gly Lys Lys Lys	
375	
agcgggtggcg tgatcacttc gcttagatta tttaactccc tgttttaact cagagctttg	1273
gtaaaagtgc gcccatgttt caagctgggg taagttagtt gtgtttgaag agattgggtg	1333
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<210> 6
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 <212> PRT
 <213> Zea mays

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 20 25 30
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 35 40 45
 Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His
 50 55 60

Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile
 65 70 75 80
 Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Asp Met Lys Lys Gln
 85 90 95
 Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu
 100 105 110
 Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser
 115 120 125
 Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg
 130 135 140
 Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala
 145 150 155 160
 Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val
 165 170 175
 Ala Ser Glu Asp Met Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu
 180 185 190
 Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile Pro Val Met Glu Phe
 195 200 205
 Asp Val Ala Lys Val Leu Glu Leu Glu Leu Thr Met Asp Gln Phe
 210 215 220
 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys
 225 230 235 240
 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser
 245 250 255
 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro
 260 265 270
 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn
 275 280 285
 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu
 290 295 300
 Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg
 305 310 315 320
 Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
 325 330 335
 Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
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 Met Gly Ile Lys Gly Leu
 1 5
 acg aaa ctg ctg gcg gac aat gcg ccc aag gcg atg aag gag cag aag 162
 Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys
 10 15 20
 ttc gag agc tac ttc ggc cgc aaa atc gcc gtc gac gcc agc atg agc 210

Phe	Glu	Ser	Tyr	Phe	Gly	Arg	Lys	Ile	Ala	Val	Asp	Ala	Ser	Met	Ser		
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Ile	Tyr	Gln	Phe	Leu	Ile	Val	Val	Gly	Arg	Thr	Gly	Met	Glu	Thr	Leu		
	40					45					50						
aca	aat	gaa	gct	ggg	gaa	gtc	act	agt	cat	ttg	caa	gga	atg	ttc	aac	306	
Thr	Asn	Glu	Ala	Gly	Glu	Val	Thr	Ser	His	Leu	Gln	Gly	Met	Phe	Asn		
	55				60					65					70		
cgg	aca	ata	aga	tta	ctg	gaa	gcg	gga	atc	aag	cca	gtt	tat	gtt	ttt	354	
Arg	Thr	Ile	Arg	Leu	Leu	Glu	Ala	Gly	Ile	Lys	Pro	Val	Tyr	Val	Phe		
				75					80					85			
gat	ggc	aag	cct	cct	gat	atg	aag	aaa	caa	gaa	ctt	gct	aaa	aga	tac	402	
Asp	Gly	Lys	Pro	Pro	Asp	Met	Lys	Lys	Gln	Glu	Leu	Ala	Lys	Arg	Tyr		
			90					95					100				
tca	aaa	aga	gat	gat	gca	acc	aaa	gat	ctg	act	gag	gca	gta	gag	gta	450	
Ser	Lys	Arg	Asp	Asp	Ala	Thr	Lys	Asp	Leu	Thr	Glu	Ala	Val	Glu	Val		
		105					110					115					
gga	gat	aaa	gat	gcg	att	gaa	aaa	ttg	agc	aag	agg	act	gta	aag	gtc	498	
Gly	Asp	Lys	Asp	Ala	Ile	Glu	Lys	Leu	Ser	Lys	Arg	Thr	Val	Lys	Val		
	120					125					130						
aca	agg	caa	cac	aac	gaa	gat	tgt	aaa	cga	cta	tta	aga	ctt	atg	ggg	546	
Thr	Arg	Gln	His	Asn	Glu	Asp	Cys	Lys	Arg	Leu	Leu	Arg	Leu	Met	Gly		
	135				140					145					150		
gtt	cct	gtt	gta	gag	gca	cct	tct	gaa	gca	gaa	gca	gaa	tgt	gca	gcc	594	
Val	Pro	Val	Val	Glu	Ala	Pro	Ser	Glu	Ala	Glu	Ala	Glu	Cys	Ala	Ala		
				155					160					165			
ctt	tgc	ata	aac	gat	aag	gtg	ttc	gct	gtt	gct	tca	gaa	gat	aag	gac	642	
Leu	Cys	Ile	Asn	Asp	Lys	Val	Phe	Ala	Val	Ala	Ser	Glu	Asp	Lys	Asp		
			170					175					180				
tcc	ctt	act	ttt	ggg	gct	cca	cgg	ttc	ctt	cgt	cat	tta	atg	gat	cca	690	
Ser	Leu	Thr	Phe	Gly	Ala	Pro	Arg	Phe	Leu	Arg	His	Leu	Met	Asp	Pro		
			185				190					195					
agt	tcc	aag	aaa	ata	cct	gtg	atg	gaa	ttt	gat	gtt	gcc	aag	gtt	ttg	738	
Ser	Ser	Lys	Lys	Ile	Pro	Val	Met	Glu	Phe	Asp	Val	Ala	Lys	Val	Leu		
	200					205					210						
gag	gag	ctt	gaa	ctc	acc	atg	gac	cag	ttc	att	gat	ttg	tgc	atc	ctg	786	
Glu	Glu	Leu	Glu	Leu	Thr	Met	Asp	Gln	Phe	Ile	Asp	Leu	Cys	Ile	Leu		
	215				220					225					230		
tgt	gga	tgt	gac	tat	tgt	gat	agc	atc	aaa	ggg	atc	ggg	ggg	caa	aca	834	
Cys	Gly	Cys	Asp	Tyr	Cys	Asp	Ser	Ile	Lys	Gly	Ile	Gly	Gly	Gln	Thr		
				235					240					245			
gct	ctg	aaa	ctt	att	cgt	caa	cat	ggg	tcc	ata	gaa	agc	atc	ttg	gag	882	
Ala	Leu	Lys	Leu	Ile	Arg	Gln	His	Gly	Ser	Ile	Glu	Ser	Ile	Leu	Glu		
			250					255					260				
aat	ctt	aat	aaa	gac	aga	tat	caa	att	cct	gag	gac	tgg	cct	tac	caa	930	
Asn	Leu	Asn	Lys	Asp	Arg	Tyr	Gln	Ile	Pro	Glu	Asp	Trp	Pro	Tyr	Gln		
		265					270					275					

gaa gct cga cgc ttg ttc aag gag cct aat gtc act ttg gat att cct	978
Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro	
280 285 290	
gag cta aaa tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg	1026
Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu	
295 300 305 310	
gta aaa gat aat ggt ttc aat gaa gat cgg gtg aca aag gcc ata gag	1074
Val Lys Asp Asn Gly Phe Asn Glu Asp Arg Val Thr Lys Ala Ile Glu	
315 320 325	
aag atc aaa tct gcc aag aat aaa tcg tcg caa gga aga ctc gag tcc	1122
Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser	
330 335 340	
ttt ttc aag cca act gcc acc aca tca gca ccg cta aaa cgg aag gag	1170
Phe Phe Lys Pro Thr Ala Thr Ser Ala Pro Leu Lys Arg Lys Glu	
345 350 355	
act tcg gat aaa aca agc aag gca gct gcg aac aag aaa aca aag gct	1218
Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala Asn Lys Lys Thr Lys Ala	
360 365 370	
ggg gga aag aag aaa taatcttgga tgcttgatgt acaactacga ctacgaaagc	1273
Gly Gly Lys Lys Lys	
375	
agcgggtggca tgatcacttc gcctagatta ttttaactccc tgttttaact cagacctttg	1333
gtgaaagtgtt gcccatgttt caagctgggg taagttagtt gtgtttgaag agattggtgt	1393
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<400> 8

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Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Val Val Gly Arg	
35 40 45	
Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His	
50 55 60	
Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile	
65 70 75 80	
Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Asp Met Lys Lys Gln	
85 90 95	
Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu	
100 105 110	
Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser	
115 120 125	
Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg	
130 135 140	
Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala	
145 150 155 160	

Glu	Ala	Glu	Cys	Ala	Ala	Leu	Cys	Ile	Asn	Asp	Lys	Val	Phe	Ala	Val
			165						170					175	
Ala	Ser	Glu	Asp	Lys	Asp	Ser	Leu	Thr	Phe	Gly	Ala	Pro	Arg	Phe	Leu
			180					185					190		
Arg	His	Leu	Met	Asp	Pro	Ser	Ser	Lys	Lys	Ile	Pro	Val	Met	Glu	Phe
		195					200					205			
Asp	Val	Ala	Lys	Val	Leu	Glu	Glu	Leu	Glu	Leu	Thr	Met	Asp	Gln	Phe
		210				215					220				
Ile	Asp	Leu	Cys	Ile	Leu	Cys	Gly	Cys	Asp	Tyr	Cys	Asp	Ser	Ile	Lys
225					230					235					240
Gly	Ile	Gly	Gly	Gln	Thr	Ala	Leu	Lys	Leu	Ile	Arg	Gln	His	Gly	Ser
				245					250					255	
Ile	Glu	Ser	Ile	Leu	Glu	Asn	Leu	Asn	Lys	Asp	Arg	Tyr	Gln	Ile	Pro
			260					265					270		
Glu	Asp	Trp	Pro	Tyr	Gln	Glu	Ala	Arg	Arg	Leu	Phe	Lys	Glu	Pro	Asn
		275					280					285			
Val	Thr	Leu	Asp	Ile	Pro	Glu	Leu	Lys	Trp	Thr	Ala	Pro	Asp	Glu	Glu
		290				295					300				
Gly	Leu	Ile	Ser	Phe	Leu	Val	Lys	Asp	Asn	Gly	Phe	Asn	Glu	Asp	Arg
305					310					315					320
Val	Thr	Lys	Ala	Ile	Glu	Lys	Ile	Lys	Ser	Ala	Lys	Asn	Lys	Ser	Ser
			325						330					335	
Gln	Gly	Arg	Leu	Glu	Ser	Phe	Phe	Lys	Pro	Thr	Ala	Thr	Thr	Ser	Ala
			340					345					350		
Pro	Leu	Lys	Arg	Lys	Glu	Thr	Ser	Asp	Lys	Thr	Ser	Lys	Ala	Ala	Ala
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Asn	Lys	Lys	Thr	Lys	Ala	Gly	Gly	Lys	Lys	Lys					
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<210> 9
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon an adaptor
 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

<400> 9
 tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa
 36

<210> 10
 <211> 380
 <212> PRT
 <213> Homo sapiens

Met	Gly	Ile	Gln	Leu	Ala	Lys	Leu	Ile	Ala	Asp	Val	Ala	Pro	Ser
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Ala	Ile	Arg	Glu	Asn	Asp	Ile	Lys	Ser	Tyr	Phe	Gly	Arg	Lys	Val
		20					25					30		
Ile	Asp	Ala	Ser	Met	Ser	Ile	Tyr	Gln	Phe	Leu	Ile	Ala	Val	Arg
		35				40					45			
Gly	Gly	Asp	Val	Leu	Gln	Asn	Glu	Glu	Gly	Glu	Thr	Thr	Ser	His
	50				55					60				
Met	Gly	Met	Phe	Tyr	Arg	Thr	Ile	Arg	Met	Met	Glu	Asn	Gly	Ile
65					70				75					80

Pro	Val	Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Gln	Leu	Lys	Ser	Gly	Glu
				85					90					95	
Leu	Ala	Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln
			100					105					110		
Gln	Ala	Gln	Ala	Ala	Gly	Ala	Glu	Gln	Glu	Val	Glu	Lys	Phe	Thr	Lys
		115					120					125			
Arg	Leu	Val	Lys	Val	Thr	Lys	Gln	His	Asn	Asp	Glu	Cys	Lys	His	Leu
	130					135					140				
Leu	Ser	Leu	Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu
145					150					155					160
Ala	Ser	Cys	Ala	Ala	Leu	Val	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala
			165						170					175	
Thr	Glu	Asp	Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg
		180						185					190		
His	Leu	Thr	Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His
	195						200					205			
Leu	Ser	Arg	Ile	Leu	Gln	Glu	Leu	Gly	Leu	Asn	Gln	Glu	Gln	Phe	Val
	210				215						220				
Asp	Leu	Cys	Ile	Leu	Leu	Gly	Ser	Asp	Tyr	Cys	Glu	Ser	Ile	Arg	Gly
225					230					235					240
Ile	Gly	Pro	Lys	Arg	Ala	Val	Asp	Leu	Ile	Gln	Lys	His	Lys	Ser	Ile
			245						250					255	
Glu	Glu	Ile	Val	Arg	Arg	Leu	Asp	Pro	Asn	Lys	Tyr	Pro	Val	Pro	Glu
		260						265					270		
Asn	Trp	Leu	His	Lys	Glu	Ala	His	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val
	275						280						285		
Leu	Asp	Pro	Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu
	290					295					300				
Glu	Leu	Ile	Lys	Phe	Met	Cys	Gly	Glu	Lys	Gln	Phe	Ser	Glu	Glu	Arg
305					310					315					320
Ile	Arg	Ser	Gly	Val	Lys	Arg	Leu	Ser	Lys	Ser	Arg	Gln	Gly	Ser	Thr
			325						330					335	
Gln	Gly	Arg	Leu	Asp	Asp	Phe	Phe	Lys	Val	Thr	Gly	Ser	Leu	Ser	Ser
		340						345					350		
Ala	Lys	Arg	Lys	Glu	Pro	Glu	Pro	Lys	Gly	Ser	Thr	Lys	Lys	Lys	Ala
	355						360					365			
Lys	Thr	Gly	Ala	Ala	Gly	Lys	Phe	Lys	Arg	Gly	Lys				
	370					375					380				

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